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REMARKS

In the Claims:

Claims 22-24 are cancelled herein without prejudice or disclaimer. Claim 25 is rewritten as an independent claim so that it no longer depends from cancelled claim 22.

Likewise, the dependency of claim 26 has been amended, such that claim 26 now depends from claim 25 rather than from cancelled claim 22. Claim 35 has been amended to correct a typographical error.

Rejections Withdrawn:

Applicants thank the Examiner for withdrawing the rejection of claims 22-27, 30-31, and 33-34 under 35 U.S.C. § 112, second paragraph; and for withdrawing the rejection of claims 22-27 and 32-34 under 35 U.S.C. § 112, first paragraph, for lack of enablement due to insufficient information regarding the deposit.

Request for Continued Examination:

Claim Rejections under 35 U.S.C. § 101

Utility:

The Examiner has maintained his rejection of claims 22-26 under 35 U.S.C. § 101, alleging that the claimed invention is not supported by either a substantial asserted utility or a well established utility. Specifically, the Examiner does not find Applicants arguments, based on the Goddard and Ashkenazi declarations to be persuasive.

Applicants respectfully disagree and maintain that the Goddard and Ashkenazi declarations demonstrate that the claimed invention is supported by both a specific, substantial, asserted utility and a well established utility.

In any event, in maintaining the rejection for lack of utility, the Examiner asserts that in the "absence (of) evidence that the polypeptide is expressed at an elevated level one would conclude that the claimed invention is not supported by either a substantial asserted utility or a well established utility." In addition, the Examiner asserts that there is no evidence of record that any nucleic acid other than SEQ ID NO:68 is amplified in

colon or lung tumors and as such there would be no specific utility for any nucleic acid encoding a polypeptide that is at least 80% identical to SEQ ID NO:69 or any nucleic acid other than SEQ ID NO:68 which encodes SEQ ID NO:69.

Applicants respectfully disagree. First, Applicants have amended the claims to encompass only those polypeptides with at least 95% sequence identity to SEQ ID NO: 69 or with at least 95% sequence identity to a polypeptide encoded by SEQ ID NO:68. Second, evidence of overexpression of the polypeptide is not required to demonstrate utility of the claimed invention.

"An applicant need only provide one credible assertion of specific and substantial utility for each claimed invention to satisfy the utility requirement." MPEP § 2107. Thus, the present invention should not be rejected for lack of utility because one of ordinary skill in the art would appreciate that the claimed polypeptides would be useful in creating degenerative oligonucleotide probes, which can be used to isolate genomic and cDNA nucleotide sequences that are amplified in lung and colon tumors. See Lodish *et. al.*, *Molecular Cell Biology* (4th ed.) 2000, Figure 7-19 (*Appendix A*).

Specific oligonucleotide probes for the gene encoding PRO357 can be synthesized chemically based on a portion of the amino acid sequence disclosed in SEQ ID NO:69. For an oligonucleotide to be useful as a probe, it must be long enough for its sequence to occur uniquely in the clone of interest and not in any other clones. The skilled artisan would appreciate that generally that means the oligonucleotide should contain at least 20 nucleic acids. In principle, probes of that length may be prepared from a sequence as short as 7 amino acids.

Degenerative oligonucleotide probes may be created by digesting PRO357 with one or more proteases into specific peptides. Based on the genetic code, the oligonucleotide sequences encoding the determined peptide sequences can be predicted. Due to the degeneracy of the genetic code, oligonucleotides containing all possible combinations of codons are synthesized to assure that at least one will match the gene perfectly. The final step is to radiolabel the oligonucleotides by transferring a ³²P-labeled phosphate group from ATP to the 5' end of each oligonucleotide. Screening a cDNA library with a

degenerate probe (created by using the polypeptide of PRO357) using membrane-hybridization techniques, will identify PRO357 nucleic acid clones that hybridize to the perfectly complementary oligonucleotide present in the probe mixture.

Use of the polypeptide sequence of PRO357 for creating oligonucleotide probes is a specific utility. "Specific utility" is defined as:

[a] utility that is *specific* to the subject matter claimed. This contrasts with a *general* utility that would be applicable to the broad class of the invention. For example, a polynucleotide whose use is disclosed simply as a 'gene probe' or 'chromosome marker' would not be considered to be *specific* in the absence of a disclosure of a specific DNA target. Similarly, a general statement of diagnostic utility, such as diagnosing an unspecified disease, would ordinarily be insufficient absent a disclosure of what condition can be diagnosed.

Revised Interim Utility Guidelines Training Materials, pgs. 5-6 (<http://www.uspto.gov/web/offices/pac/utility/utilityguide.pdf>). Utility of the presently claimed polypeptide for generating oligonucleotide probes is specific because such an oligonucleotide probe would be useful for identifying and isolating the nucleic acid encoding the claimed polypeptide. It is undisputed that the nucleic acid (SEQ ID NO:68) encoding the claimed polypeptide is amplified in lung and colon tumors and therefore, has a specific diagnostic utility. See pages 119-137 of the specification describing the gene amplification experiments. Thus, the presently claimed polypeptide has the specific utility of generating a probe capable of identifying and isolating the nucleic acid encoding it, where the nucleic acid has a diagnostic utility because it is amplified in lung and colon tumors.

Use of the polypeptide sequence of PRO357 for creating oligonucleotide probes is also a substantial utility. "Substantial utility" is defined as:

a utility that defines a 'real world' use. Utilities that require or constitute carrying out further research to identify or reasonably confirm a "real world" context of use are not substantial utilities. For example, both a therapeutic method of treating a known or newly discovered disease and an assay method for identifying compounds that themselves have a "substantial utility" define a "real world" context of use. An assay that measures the presence of a material which has a stated correlation to a predisposition to the onset of a particular disease condition

would also define a "real world" context of use in identifying potential candidates for preventive measure or further monitoring.

Revised Interim Utility Guidelines Training Materials, pg. 6 (<http://www.uspto.gov/web/offices/pac/utility/utilityguide.pdf>). Utility of the presently claimed polypeptide for generating oligonucleotide probes is substantial because such an oligonucleotide probe would be useful for identifying and isolating the nucleic acid encoding the claimed polypeptide. It is undisputed that the nucleic acid (SEQ ID NO:68) encoding the claimed polypeptide is amplified in lung and colon tumors and therefore, has a substantial diagnostic utility. See pages 119-137 of the specification describing the gene amplification experiments. Thus, the presently claimed polypeptide has the substantial utility of generating a probe capable of identifying and isolating the nucleic acid encoding it, where the nucleic acid has a diagnostic utility because it is amplified in lung and colon tumors.

Further, use of the polypeptide sequence of PRO357 for creating oligonucleotide probes is a credible utility:

Where an applicant has specifically asserted that an invention has a particular utility, that assertion cannot simply be dismissed by Office personnel as being 'wrong'. Rather, Office personnel must determine if the assertion of utility is credible (*i.e.*, whether the assertion of utility is believable to a person of ordinary skill in the art based on the totality of evidence and reasoning provided). An assertion is credible unless (A) the logic underlying the assertion is seriously flawed, or (B) the facts upon which the assertion is based are inconsistent with the logic underlying the assertion. Credibility as used in this context refers to the reliability of the statement based on the logic and facts that are offered by the applicant to support the assertion of utility. A *credible* utility is assessed from the standpoint of whether a person of ordinary skill in the art would accept that the recited or disclosed invention is currently available for such use. For example, no perpetual motion machines would be considered to be currently available. However, nucleic acids could be used as probes, chromosome markers, or forensic or diagnostic markers. Therefore the credibility of such an assertion would not be questioned, although such a use might fail the *specific* and *substantial* tests.

Revised Interim Utility Guidelines Training Materials, pg. 5 (<http://www.uspto.gov/web/offices/pac/utility/utilityguide.pdf>). Utility of the presently claimed polypeptide for generating oligonucleotide probes is credible because neither the logic underlying this

assertion is flawed, nor are the facts inconsistent with this logic. Moreover, the Utility Guidelines specifically recognize probes as having a credible utility.

Finally, use of the polypeptide sequence of PRO357 for creating oligonucleotide probes is a well-established utility. A "well established" utility is a:

specific, substantial, and credible utility which is well known, immediately apparent, or implied by the specification's disclosure of the properties of the material, alone or taken with the knowledge of one skilled in the art.

Revised Interim Utility Guidelines Training Materials, pg. 7 (<http://www.uspto.gov/web/offices/pac/utility/utilityguide.pdf>). Utility of the presently claimed polypeptide for generating oligonucleotide probes is well established because it is implied by the specification's disclosure, and would be immediately apparent to one of ordinary skill in the art. At page 16, lines 3-5 of the specification, Applicants assert that "oligonucleotide probes (are) useful for isolating genomic and cDNA nucleotide sequences or as antisense probes." The gene amplification experiment, described at pages 119-137 of the application, demonstrates the specific diagnostic utility (for lung and colon tumors) of the nucleic acid encoding PRO357. At the time the application was filed, it was well known to one of ordinary skill in the art to use a polypeptide sequence to generate oligonucleotide probes capable of identifying and isolating a nucleic acid sequence of interest, such as the nucleic acid sequence encoding PRO357. See Lodish *et. al.*, *Molecular Cell Biology* (4th ed.) 2000, Figure 7-19 and Chapter 7.3 (Appendix A).

For all the above reasons, Applicants have demonstrated currently pending claims 25-26 are supported by an asserted substantial, and specific utility as well as by a well-established utility. Therefore, Applicants respectfully request that the Examiner withdraw the rejection of claims 25-26 for lack of utility.

35 U.S.C. § 112 ¶ 1, Enablement-Utility

The Examiner has rejected claims 22-36 under 35 U.S.C. § 112 ¶1, alleging that because the claimed invention is not supported by either a specific asserted utility or a well established utility, one skilled in the art would not know how to use the claimed invention. As discussed in the remarks above, addressing the rejection under 35 U.S.C.

§ 101 for lack of utility, Applicants respectfully submit that the claimed polypeptide has the specific, substantial, and credible utility of generating degenerative oligonucleotide probes, which can be used to isolated the amplified genomic and cDNA nucleotide sequences discussed in the gene amplification experiments at pages 119-137 of the specification. Further, Applicants disclose, at Example 14, pages 106-107, that protein sequences were used to search various databases and then used to create a consensus DNA sequence that was used as a probe to isolate a clone of the full-length coding sequence of PRO357. Moreover, generation of and use of degenerative oligonucleotide probes was well known by the time the application was filed. For example, Watson *et al.*, describe using a 32 amino acid sequence from the urate oxidase protein to design two degenerate oligonucleotide probes which were then used in a PCR reaction that resulted in a unique probe capable of hybridizing to a full length cDNA for urate oxidase. See Watson, *et al.*, *Recombinant DNA* (2nd ed.) 1992, Figure 7-7 (*Appendix B*). Thus, one of ordinary skill in the art would be enabled to use the present invention to generate oligonucleotide probes capable of hybridizing to nucleic acid sequences that are amplified in lung and colon tumors. Applicants respectfully request the Examiner reconsider and withdraw the rejection of claims 22-36 under 35 U.S.C. § 112 ¶1 for their alleged inadequate disclosure on how to use the claimed invention.

Claim rejections under 35 U.S.C. § 112, first paragraph

Written Description:

The Examiner has maintained his rejection of Claims 22-26 and 33-34 under 35 U.S.C. § 112, first paragraph, contending that they contain subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. Applicants respectfully disagree.

Applicants previously argued that the specification conveys to one skilled in the art that Applicants had possession of the claimed invention at the time the application was filed

because Applicants disclosed several structural and functional features of the claimed sequences. The Examiner rejected this argument, stating that disclosure of such structural features does not lead to possession of nucleic acids as broadly claimed where the specification does not disclose any polypeptides that are 80-99% identical to SEQ ID NO:69 or to polypeptides encoded by SEQ ID NO:68.

Applicants respectfully disagree. Applicants have cancelled claims 22-24 without prejudice or disclaimer. Therefore, Applicants' claims are now directed to nucleic acids that are 95-99% identical to the polypeptide disclosed in the specification, SEQ ID NO:69. Moreover, both Examples 13 and 14 from the revised Interim Written Description Guidelines Training Materials, published at <http://www.uspto.gov/web/menu/written.pdf>, state that an adequate description of a genus of sequences includes a description of structural features common to the genus. As Applicants previously argued, Applicants have disclosed such common structural features at page 107, lines 14-20 of the specification, as well as at Figure 26. However, Applicants do not rely on their description of common structural features alone.

Applicants also previously compared the exemplary adequate written description found in Example 14 of the Training Materials with the disclosure of the present specification and demonstrated that the two descriptions are analogous. Specifically, like the disclosure of Example 14, Applicants' specification discloses and reduces to practice a polypeptide recited in Claims 25-26 (SEQ ID NO:69), and in addition, Applicants describe a nucleic acid sequence encoding PRO357. Like Example 14, the nucleic acids of Claims 25-26 do not vary substantially from disclosed SEQ ID NO:68 because they have 95-99% sequence identity with SEQ ID NO:69 and share common structural features with SEQ ID NO:69. Moreover, Claims 25-26 require the claimed genus of polypeptides to all have the functional feature of being encoded by nucleic acids that are amplified in lung and colon tumors.

The Examiner disagrees that Applicants' disclosure is analogous to Example 14 of the Training Materials and instead contends that overexpression in lung and colon tumors is

only the "function" of SEQ ID NO:68, and argues that the specification does not disclose any other polypeptides or how one would find a polypeptide that is 80-99% identical that would be encoded by a nucleic acid that is amplified in lung or colon tumors. The Examiner further contends that although the specification teaches a method to assay for expression, that method requires the use of the nucleic acid of the PRO or use of an antibody to the protein of SEQ ID NO:69. Finally, the Examiner argues that the specification does not teach how one would or could find any other polypeptide that is 80-99% identical to SEQ ID NO:69, which is encoded by a nucleic acid that is amplified in lung or colon tumors; nor, the Examiner contends, does the specification teach which regions or parts of the nucleic acid of SEQ ID NO:68 would be used to find such.

Applicants respectfully disagree. One of skill in the art, after reading the specification, would be able to find a polypeptide that is 95-99% identical to SEQ ID NO:69, and that is encoded by a nucleic acid that is amplified in lung or colon tumors. First, the specification, at pages 122-124, teaches that PRO357 and the nucleic acid encoding it may be isolated from lung and colon cancer tissues. One of skill in the art would appreciate that polypeptides and nucleic acids that are 95-99% identical to SEQ ID NO:68 or SEQ ID NO:69 might also be isolated from lung and colon cancer tissues. At pages 23-29, at Table 1, and at pages 34-54, the specification teaches one of skill in the art how to determine whether a particular sequence is 95-99% identical to a given sequence. Finally, as the Examiner notes, the specification, at pages 124-137, teaches a method for assaying for gene amplification in lung and colon tumors. Hence, the specification does describe how one would find a polypeptide that is 95-99% identical to SEQ ID NO:69 and also teaches how to determine whether such a polypeptide is encoded by a nucleic acid that is amplified in lung or colon tumors.

Moreover, even if the Examiner maintains that the present specification and claims are not analogous to Example 14 from the Training Materials, the Training Materials still support the conclusion that the written description requirement is satisfied for Claims 25 and 26. Specifically, Claims 25 and 26 are adequately described under the analysis of Example 13, which sets forth an exemplary adequate written description for a claim to a

genus of isolated proteins having a particular sequence, and which illustrates what is lacking in the description for a claim to genus of variants of the proteins having a particular sequence. The latter claim in Example 13 of the Training Materials is analogous to Claims 25 and 26 of the present application. According to Example 13 of the Training Materials, a claim to "[a]n isolated variant of the protein of claim 1" is not adequately described if: (1) the specification and claim do not indicate what distinguishing attributes are shared by members of the claimed genus, (2) the specification and claim do not place any limit on the number of amino acid substitutions, deletions, insertions and/or additions, and (3) the specification and claim fail to disclose structural features that could distinguish compounds in the genus from those outside the genus. The Examiner's rejection of Claims 25 and 26 is not proper because the present specification and claim do indicate distinguishing attributes that are shared by members of the claimed genus, for example, being encoded by a nucleic acid that is amplified in lung or colon tumors; the present specification and claims do limit the number of substitutions, deletions, insertions, and/or additions by requiring all sequences within the genus to be 95-99% identical to SEQ ID NO:69; and the present specification at page 107 and Figure 26 discloses several structural features common to species falling within the claimed genus. Hence, both Examples 13 and 14 of the Training Materials indicate that the present disclosure adequately describes the claimed genus. Therefore, Applicants respectfully request the Examiner withdraw this ground of rejection.

Enablement:

The Examiner has also maintained his rejection of Claims 22-36 under 35 U.S.C. § 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to make and/or use the invention.

Applicants previously argued that the specification teaches that the nucleic acid encoding PRO357 is amplified in lung or colon tumors and that one of ordinary skill in the art would be able to make variant sequences, based on the teachings at pages 59-

62 of the specification. In response, the Examiner contends that the specification teaches only SEQ ID NO:68 as being amplified in lung or colon tumors, and does not disclose any other nucleic acid or variant with that function. The Examiner maintains that, because the specification does not teach which regions to alter and still obtain expression, it would require more than routine experimentation to determine which changes to the polypeptide could be made to obtain a functional polypeptide that is encoded by a nucleic acid that is amplified in lung and colon tumors.

Applicants respectfully disagree. In *In re Wands*, 858 F.2d 731, 737 (Fed. Cir. 1988), the Federal Circuit stated:

The determination of what constitutes undue experimentation in a given case requires the application of a standard of reasonableness, having due regard for the nature of the invention and the state of the art (citations omitted). The test is not merely quantitative, since a *considerable amount of experimentation is permissible, if it is merely routine, or if the specification provides a reasonable amount of guidance* with respect to the direction in which the experimentation should proceed (emphasis added).

In order to determine whether any required experimentation is undue, the Federal Circuit set forth the following factors for consideration: (1) the nature of the invention; (2) the state of the prior art; (3) the relative skill of those in the art; (4) the level of predictability in the art; (5) the existence of working examples; (6) the breadth of the claims; (7) the amount of direction or guidance by the inventor; and (8) the quantity of experimentation needed to make or use the invention. *In re Wands*, 858 F.2d 731, 737 (Fed. Cir. 1988).

Although in the present case some experimentation might be required to practice the full scope of the claimed invention, consideration of the above factors demonstrates that such experimentation would not be undue. Specifically, the following analysis demonstrates that the specification provides a reasonable amount of guidance with respect to the direction in which any experimentation should proceed.

(1) – *Nature of the Invention*

Claimed herein are a well defined class of polypeptides, each having the characteristic of being encoded by a nucleic acid that is amplified in lung and colon tumors, and in addition, each having at least 95% sequence identity to the nucleic or amino acid sequence of PRO357.

(2) – State of the Prior Art

The state of the prior art is advanced. Analysis of the prior art as of the effective filing date of the present application shows that skilled artisans are able to routinely produce, isolate, and analyze nucleic and amino acid sequences. In addition, skilled artisans routinely perform various functional assays.

(3) – Relative Skill of those in the Art

The relative skill of those in the art is advanced.

(4) – Level of Predictability in the Art

The Examiner asserts that the art is unpredictable, alleging that because the specification does not teach which regions of the disclosed sequence to alter and still obtain expression, it would require more than routine experimentation to determine which changes to the polypeptide could be made to obtain a functional polypeptide that is encoded by a nucleic acid that is amplified in lung and colon tumors.

Applicants respectfully disagree. The level of predictability in the art of the claimed subject matter is not high. According to MPEP 2164.01(b), "the 'predictability or lack thereof' in the art refers to the ability of one skilled in the art to extrapolate the disclosed or known results to the claimed invention. If one skilled in the art can readily anticipate the effect of a change within the subject matter to which the claimed invention pertains, then there is predictability in the art."

Even though Applicants do not specifically state which portions of the disclosed wild type sequence might be altered yet still lead to a functional polypeptide that is encoded by a nucleic acid that is amplified in lung and colon tumors and that has at least 95%

sequence identity to the nucleic or amino acid sequence of PRO357, obtaining such a sequence variant is not unpredictable. The specification not only tells one of skill in the art how to produce a sequence variant (see page 61, stating that site-directed mutagenesis, cassette mutagenesis or restriction selection mutagenesis might be used to produce a nucleic acid sequence variant) but also tells one of skill in the art how to anticipate the effect of certain alterations that might be made to the wild type sequence when producing a variant sequence.

For example, site-directed mutagenesis might be used to create a variant sequence by replacing the alanine residue at amino acid 73 of Figure 26 with a valine residue. Hence, alanine, encoded by "GCA" in the nucleic acid sequence could be altered by replacing the cytosine residue with a uracil residue, to read "GUA," such that the nucleic acid sequence would then encode valine. One of skill in the art would appreciate that replacing an alanine residue with a valine residue would conserve the polypeptide structure because each of these amino acids have hydrophobic side chains. Table 6, on page 61, and the accompanying text provide more detail regarding why this modification to the sequence would conserve the structure and function of the encoded polypeptide.

In addition, Applicants disclose at page 59; lines 24-27 of the specification that "[g]uidance in determining which amino acid residues may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology." Applicants disclose at pages 6, 7, and 107 that portions of the amino acid sequence of the full-length of PRO357 possess significant homology to the acid labile subunit of insulin-growth factor. Therefore, one of ordinary skill in the art, reading the disclosure, would know to compare the claimed polypeptide sequence with the sequence for the acid labile subunit and minimize amino acid changes in regions of high homology between the sequences. Thus, based on the teachings of the specification one of skill

in the art would be able to predictably anticipate alterations made to the wild type sequences of PRO357.

(5) – *Existence of Working Examples*

According to MPEP § 2164.01(b), “as long as the specification discloses at least one method for making and using the claimed invention that bears a reasonable correlation to the entire scope of the claim, then the enablement requirement of 35 U.S.C. § 112 is satisfied. *In re Fisher*, 427 F.2d 833, 839, 166 USPQ 18, 24 (CCPA 1970).” Applicants disclose at least one method for making and using the claimed invention. In particular, Applicants disclose a polypeptide having SEQ ID NO:69 and describe in Figure 26 and at page 107 numerous characteristics of PRO357. Further, Applicants disclose that SEQ ID NO:69 is encoded by a nucleic acid that is amplified in lung or colon tumors. Specifically, Example 28, found at pages 119-137 of the specification, describes the isolation and characterization of SEQ ID NO:68 (the nucleic acid encoding SEQ ID NO:69) from lung and colon tumor tissue samples. In addition, Example 28 describes various assays and analyses conducted to determine that SEQ ID NO:68 is amplified in lung and colon tumors. According to MPEP §2164.02(b) “failure to disclose other methods by which the claimed invention may be made does not render a claim invalid under 35 U.S.C. 112. *Spectra-Physics, Inc. v. Coherent, Inc.*, 827 F.2d 1524, 1533, 3 USPQ2d 1737, 1743 (Fed. Cir.), *cert. denied*, 484 U.S. 954 (1987).”

(6) – *Breadth of the Claims*

Claims 25-36 are not overly broad. Instead they are directed to polypeptides that do not substantially vary from one another because all claimed polypeptides must have at least 95% sequence identity with either the nucleic or amino acid of PRO357, and all must be encoded by a nucleic acid that is amplified in lung and colon tumors.

(7) – *Amount of Direction or Guidance by the Inventor*

Applicants have provided a significant amount of guidance in the specification. For example, the specification describes physical and structural features of the nucleic acid. At page 107, the specification discloses various structural features, such as positioning

of the single opening reading frame, apparent translation initiation site, and positioning of the stop codon. At pages 119-124, the specification describes isolating PRO357 from various human lung and colon tissue samples. In addition, at page 7, the specification discloses that PRO357 polypeptides are proteins with leucine rich repeats having homology to the acid labile subunit of insulin-like growth factor. Table 19, on page 135, discloses framework markers for the DNA encoding PRO357 and Table 20, on page 135 the specification discloses epicenter markers for the DNA encoding PRO357 along chromosome 16. Figure 26 also describes where various structures, such as signal sequences, transmembrane domains, N-glycosylation sites, tyrosine kinase phosphorylation sites, N-myristoylation sites, prokaryotic membrane lipoprotein lipid attachment sites, EGF-like domain cysteine pattern signature sites, and leucine zipper pattern sites, are encoded.

One important characteristic of the claimed polypeptides is that they are encoded by nucleic acids that are amplified in lung or colon tumors. Page 69 of the specification discloses that the polypeptides of the invention "may be recovered from culture medium or from host cell lysates." Applicants also disclose at page 69 various methods for purifying the polypeptides of the invention. In addition, Applicants disclose that gene amplification "may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA, dot blotting, or *in situ* hybridization using an appropriately labeled probe, based on the sequences provided herein." Example 28, found at pages 119-137 of the specification, shows that PRO357-encoding genes are amplified in the genome of lung and colon tumors and cell lines.

Hence, Applicants submit that the specification provides a reasonable amount of guidance, and suggests in which direction any necessary experimentation should proceed.

In addition, at pages 23-29 and at Table 1, pages 34-54, the specification teaches one of skill in the art how to determine whether a particular sequence is 95-99% identical to

a given sequence such as SEQ ID NO:68. Finally, the specification, at pages 124-137, teaches a method for assaying a variant sequence for the function of amplification in lung and colon tumors.

(8) – Quantity of Experimentation Needed to Make or Use the Invention

Hence, although some experimentation might be required to practice the claimed invention, the specification provides sufficient guidance to enable one of ordinary skill in the art not only to make variants of SEQ ID NOS:68 and 69, but also to select variants that are amplified in lung and colon tumors. Applicants again note that even a “considerable amount of experimentation is permissible, if it is merely routine or if the specification provides a reasonable amount of guidance with respect to the direction in which the experimentation should proceed.” *In re Wands*, 858 F.2d 731,737 (Fed. Cir.1988).

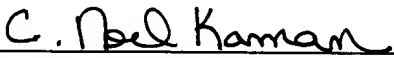
Accordingly, Applicants respectfully request that the Examiner withdraw his rejection of Claims 25-36 under 35 U.S.C. § 112, first paragraph for lack of enablement.

Appl. No. 09/943,780
Amdmt. dated 8 April 2004
Reply to Office Action of 5 February 2004

Conclusion

Applicants believe that currently pending Claims 25-36 are patentable. Applicants respectfully request the Examiner grant allowance of this application. The Examiner is invited to contact the undersigned attorney for Applicants via telephone if such communication would expedite the prosecution this application.

Respectfully submitted,


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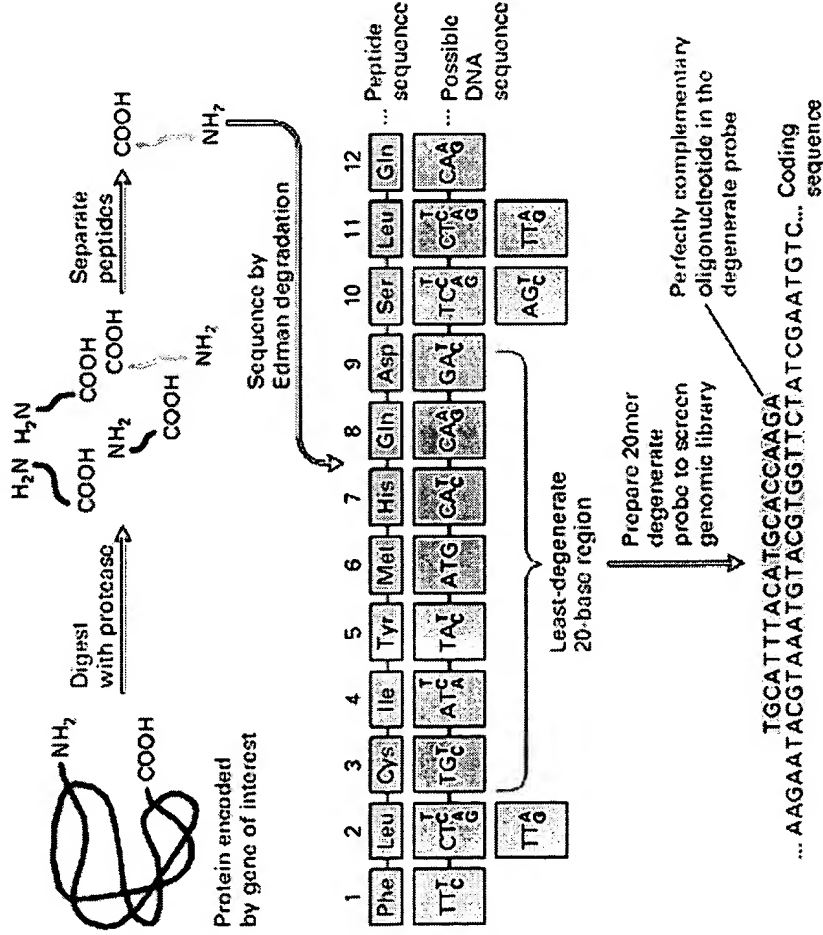


Figure 7-19. Designing oligonucleotide probes based on protein sequence. An isolated protein is digested with a selective protease such as trypsin, which specifically cleaves peptide bonds on the

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carboxy-terminal side of lysine and arginine residues. The resulting peptides are separated, and several are partially sequenced from their N-terminus by sequential Edman degradation. The determined sequences then are analyzed to identify the 6- or 7-aa region that can be encoded by the smallest number of possible DNA sequences. Because of the degeneracy of the genetic code, the 12-aa sequence (light green) shown here theoretically could be encoded by any of the DNA triplets below it, with the possible alternative bases at the same position indicated. For example, Phe-1 is encoded by TTT or TTC; Leu-2 is encoded by one of six possible triplets (CTT, CTC, CTA, CTG, TTA, or TTG). The region with the least degeneracy for a sequence of 20 bases (20-mer) is indicated by the red bracket. There are 48 possible DNA sequences in this 20-base region that could encode the peptide sequence 3 – 9. Since the actual sequence of the gene is unknown, a degenerate 20-mer probe consisting of a mixture of all the possible 20-base oligonucleotides is prepared. If a cDNA or genomic library is screened with this degenerate probe, the one oligonucleotide that is perfectly complementary to the actual coding sequence (blue) will hybridize to it.

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[7.3. Identifying, Analyzing, and Sequencing Cloned DNA](#)

Suppose you have isolated a particular protein and want to isolate the gene that encodes it. A complete genomic λ library from mammals contains at least a million different clones; a cDNA library must contain as many clones to include the sequences of scarce mRNAs. How are specific clones of interest identified in such large collections? The most common method involves screening a library by hybridization with radioactively labeled DNA or RNA probes. In an alternative method, a specific clone in a library of cloned DNA is identified based on some property of its encoded protein.

Once a particular genomic DNA or cDNA clone of interest has been identified and isolated from other clones, the cloned DNA can be separated from the vector DNA and analyzed. This separation is achieved by cleaving the recombinant vector with the same restriction enzyme used to insert the DNA fragment initially. During ligation of a cut vector and DNA fragments generated with the same restriction enzyme, the restriction recognition sequence is regenerated between the DNA fragments and vector (see [Figure 7-8](#)). Subsequent treatment with the same restriction enzyme will cut the recombinant vector at the same sites, releasing the vector and cloned DNA, which then can be separated by gel electrophoresis.

The most complete characterization of a cloned DNA requires determination of its nucleotide sequence; from this sequence, the amino acid sequence of an encoded protein can be deduced. The sequence of genomic DNA includes introns as well as exons; it also includes regions that control gene expression by determining the type of cell in which the encoded protein is expressed, the stage in development it is expressed, and the amount of protein produced. Genomic DNAs also include replication origins and sequences important in determining how the DNA associates with proteins in chromosomes. In subsequent chapters, we consider how cells use DNA sequences for these functions. In this section, techniques for identifying, characterizing, and finally sequencing cloned DNA are outlined.

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Libraries Can Be Screened with Membrane-Hybridization Assay

As discussed in Chapter 4, under the conditions of temperature and ion concentration found in cells, DNA is maintained as a duplex (double-stranded) structure by the hydrogen bonds between A · T and G · C base pairs (see Figure 4-4b). DNA duplexes can be denatured (melted) into single strands by heating them in a dilute salt solution (e.g., 0.01 M NaCl), or by raising the pH above 11. If the temperature is lowered and the ion concentration in the solution is raised, or if the pH is lowered to neutrality, the A · T and G · C base pairs re-form between complementary single strands (see Figure 4-8). This process goes by many names: renaturation, reassociation, hybridization, annealing. In a mixture of nucleic acids, only complementary single strands (or strands containing complementary regions) will reassociate; the extent of their reassociation is virtually unaffected by the presence of noncomplementary strands. Such *molecular hybridization* can take place between two complementary strands of either DNA or RNA, or between an RNA strand and a DNA strand.

To detect specific DNA clones by molecular hybridization, cloned recombinant DNA molecules are denatured and the single strands attached to a solid support, commonly a nitrocellulose filter or treated nylon membrane (Figure 7-17). When a solution containing single-stranded nucleic acids is dried on such a membrane, the single strands become irreversibly bound to the solid support in a manner that leaves most of the bases available for hybridizing to a complementary strand. Although the chemistry of this irreversible binding is not well understood, the procedure is very useful. The membrane is then incubated in a solution containing a radioactively labeled single-stranded DNA (or RNA) *probe* that is complementary to some of the nucleic acid bound to the membrane. Under hybridization conditions (near neutral pH, 40 – 65 °C, 0.3 – 0.6 M NaCl), this labeled probe hybridizes to the complementary nucleic acid bound to the membrane. Any excess probe that does not hybridize is washed away, and the labeled hybrids are detected by autoradiography of the filter.

The procedure for screening a λ library with this membrane-hybridization technique is outlined in Figure 7-18. The recombinant λ virions present in plaques on a lawn of *E. coli* are transferred to a nylon membrane by placing the membrane on the surface of the petri dish. Many of the viral particles in each plaque adsorb to the surface of the membrane, but many virions remain in the plaques on the surface of the nutrient agar in the petri dish. In this way a *replica* of the petri dish containing a large number of individual λ clones is reproduced on the surface of the membrane. The original petri dish is refrigerated to store the collection of λ clones. The membrane is then incubated in an alkaline solution, which disrupts the virions, releasing and denaturing the encapsulated DNA. The membrane is then dried, fixing the recombinant λ DNA to the membrane's surface. Next, the membrane is incubated with a radiolabeled probe under hybridization conditions. Unhybridized probe is washed

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away, and the filter is subjected to autoradiography.

The appearance of a spot on the autoradiogram indicates the presence of a recombinant λ clone containing DNA complementary to the probe. The position of the spot on the autoradiogram corresponds to the position on the original petri dish where that particular clone formed a plaque. Since the original petri dish still contains many infectious virions in each plaque, viral particles from the identified clone can be recovered for replating by aligning the autoradiogram and the petri dish and removing viral particles from the clone corresponding to the spot. A similar technique can be applied for screening a plasmid library in *E. coli* cells. [↑ top](#)


Oligonucleotide Probes Are Designed Based on Partial Protein Sequences


Identification of specific clones by the membrane-hybridization technique depends on the ability to prepare specific, radiolabeled probes. Specific oligonucleotide probes for the gene encoding a protein of interest can be synthesized chemically if a portion of the amino acid sequence of the protein is determined. For an oligonucleotide to be useful as a probe, it must be long enough for its sequence to occur uniquely in the clone of interest and not in any other clones. For most purposes, this condition is satisfied by oligonucleotides containing about 20 nucleotides. This is because a specific 20-nucleotide sequence occurs once in every 4^{20} ($\approx 10^{12}$) nucleotides. Since all genomes are much smaller ($\approx 3 \times 10^9$ nucleotides for humans), a specific 20-nucleotide sequence in a genome usually occurs only one time. In principle, probes this length can be prepared based on only a 7-aa sequence out of a protein's total sequence (20 nucleotides $\div 3$ nucleotides per codon ≈ 7 amino acids). However, a somewhat longer amino acid sequence usually is determined to allow the preparation of several probes for use in cloning a gene of interest.


Here we describe two different approaches for preparing oligonucleotide probes. Generally, a radiolabeled oligonucleotide probe is used to screen a λ cDNA library using the membrane-hybridization technique. Once a cDNA clone encoding a particular protein is obtained, the full-length radiolabeled cDNA can be used to probe a genomic library for clones that contain fragments of the gene encoding the protein.


Degenerate Probes

One method for preparing a specific probe is outlined in [Figure 7-19](#). The purified protein of interest is digested with one or more proteases (e.g., trypsin) into specific peptides, and the N-terminal amino acid sequences of a few of these peptides is determined by sequential Edman degradation or mass

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spectrometry (see [Figures 3-46 and 3-47](#)). Based on the genetic code, the oligonucleotide sequences encoding the determined peptide sequences can be predicted. Recall, however, that the genetic code is degenerate; that is, many amino acids are encoded by multiple codons (see [Table 4-2](#)). Since the specific codons used to encode the protein of interest are unknown, oligonucleotides containing all possible combinations of codons must be synthesized to assure that one of them will match the gene perfectly.


Once several peptides have been sequenced, the 6- or 7-aa stretch that can be encoded by the smallest number of possible DNA sequences is determined. For example, as illustrated in [Figure 7-19](#), the amino acids in the sequence extending from position 3 through 8 (Cys-Ile-Tyr-Met-His-Gln) can be encoded by 2, 3, 2, 1, 2, and 2 possible codons, respectively. Consequently, $48 (= 2 \times 2 \times 1 \times 2 \times 2)$ different 18-base DNA sequences could encode this one sequence of amino acids. The GA added at the 3' end of these 18-base sequences must be complementary to the gene since the next amino acid in this peptide, Asp-9, is encoded by two codons that both start with GA. To be certain of obtaining a probe based on this amino acid sequence that hybridizes perfectly to the unique sequence present in the gene, all 48 of the 20-mer probes must be synthesized. A mixture of 20-mer probes based on any other portion of this peptide sequence would have to contain considerably more than 48 oligonucleotides because of the presence of leucine or serine residues, each encoded by six different codons.

A mixture of all the oligonucleotides that can encode a selected portion of a peptide sequence is called a *degenerate probe*. Such a mixture can be prepared at one time by adding more than one nucleotide precursor to the synthesis reaction at those points in the sequence that can be encoded by alternative bases. The final step in preparing this type of probe is to radiolabel the oligonucleotides, usually by transferring a ^{32}P -labeled phosphate group from ATP to the 5' end of each oligonucleotide using *polynucleotide kinase* ([Figure 7-20](#)). Screening of a λ cDNA library with a degenerate probe using the membrane-hybridization technique will identify clones that hybridize to the perfectly complementary oligonucleotide present in the probe mixture. Under the usual experimental conditions, oligonucleotides that differ from the cDNA sequence at one or two bases also will hybridize. [↑ top](#)

Unique EST-Based Probes

In recent years another approach has become available for obtaining a probe based on the partial amino acid sequence determined from an isolated protein. Because this approach utilizes cDNA sequence data, it identifies a single oligonucleotide, rather than a degenerate mixture, that can be used to screen a library for a particular gene. Using methods for DNA sequencing described later,

researchers have sequenced portions of vast numbers of cDNAs isolated from human cells and some additional important model organisms such as the mouse, *Drosophila*, and the roundworm *Caenorhabditis elegans*. These partial cDNA sequences, generally 200 to 400 bp in length, have been stored in computers and are available to researchers throughout the world via the Internet, the international computer network. This collection of partial cDNA sequences is called the *expressed sequence tag (EST)* database because it is composed of relatively short portions (tags) of genomic DNA sequence that are expressed in the form of mRNA. The EST database is constantly updated as sequences from increasing numbers of cDNA clones are added to it.

Computer programs that apply the genetic code are used to translate the EST sequences into partial protein amino acid sequences. Using programs that have been developed for the purpose and a personal computer, a researcher can search the current EST database for an EST that encodes a specific partial amino acid sequence in the particular protein under study. If a match is found, then the EST provides the unique DNA sequence of that portion of the full-length cDNA. A single, specific probe up to ≈ 100 bases long that is perfectly complementary to a portion of the EST can then be synthesized and radiolabeled. Alternatively, the polymerase chain reaction, described at the end of the chapter, can be used to synthesize a probe equal to the full length of the EST. By now, the human EST database is so large that ESTs can be identified that encode partial amino acid sequences determined from most isolated human proteins. 

Specific Clones Can Be Identified Based on Properties of the Encoded Proteins

Genomic and cDNA libraries can also be screened for the properties of a specific protein encoded in the cloned DNA. This approach uses special cloning vectors, called λ expression vectors, in which the cloned DNA is transcribed into mRNA, which in turn is translated into the encoded protein. For example, λ phage vectors have been constructed so that the junction of inserted DNA lies in a region of the vector that is transcribed and translated at a high rate. Cloned DNA inserted at this position is transcribed into mRNA in every cell infected by this type of vector. If the cloned DNA contains a protein-coding sequence inserted in the same reading frame as the vector protein, infected cells will produce a *fusion protein* in which the amino terminus is encoded by the vector DNA and the remainder of the molecule by the cloned DNA ([Figure 7-21](#)).

When replica nitrocellulose filters are prepared from a recombinant library constructed in a λ expression vector, fusion proteins expressed from each individual clone are bound to the nitrocellulose filter. The replica filter can be screened by procedures capable of detecting specific fusion proteins. For example, a monoclonal antibody specific for a protein of interest can be incubated with replica

filters of a λ cDNA expression library. If one of the λ clones expresses a fusion protein that includes the region of the protein bound by that monoclonal antibody, antibody molecules will bind to the filter at the position of that specific clone. After washing of the filter to remove unbound antibody, the position of the specific clone is detected by incubation with a second radioactively labeled antibody that recognizes the first antibody, followed by autoradiography of the filter.

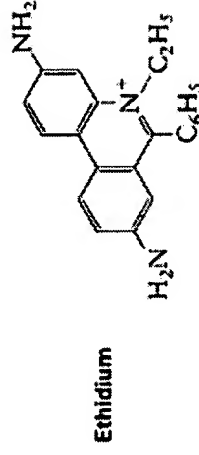
In this method, termed expression cloning, any molecule that binds to a protein of interest with high affinity and specificity can be labeled and used as a probe to identify clones expressing the interacting protein. For instance, expression cloning has been useful in identifying cDNA clones encoding proteins that bind to specific DNA sequences; many such proteins are involved in controlling transcription. In this case, a labeled synthetic double-stranded DNA probe is incubated with replica filters prepared from a cDNA library cloned into a λ expression vector. Binding of the labeled DNA by fusion proteins locates the positions of desired clones on the original filter. As described in a later section, other types of expression vectors can be used to produce large amounts of a protein from a cloned gene. [↑ top](#)

Gel Electrophoresis Resolves DNA Fragments of Different Size

Once a specific DNA clone has been isolated, the cloned DNA is separated from the vector DNA by cleavage with the restriction enzyme used to form the recombinant plasmid, as described earlier. The cloned DNA and vector DNA then are separated by gel electrophoresis, a powerful method for separating proteins according to size ([Chapter 3](#)). Gel electrophoresis also is used to separate DNA and RNA molecules by size and to estimate the size of nucleic acid molecules of unknown length by comparison with the migration of molecules of known length.

DNA and RNA molecules are highly charged near neutral pH because the phosphate group in each nucleotide contributes one negative charge. As a result, DNA and RNA molecules move toward the positive electrode during gel electrophoresis. Smaller molecules move through the gel matrix more readily than larger molecules, so that molecules of different length, such as restriction fragments, separate ([Figure 7-22](#)). Because the gel matrix restricts random diffusion of the molecules, molecules of different length separate into "bands" whose width equals that of the well into which the original DNA mixture was placed. The resolving power of gel electrophoresis is so great that single-stranded DNA molecules up to about 500 nucleotides long can be separated if they differ in length by only 1 nucleotide. This high resolution is critical to the DNA-sequencing procedures described later. DNA molecules composed of up to ≈ 2000 nucleotides usually are separated electrophoretically on *polyacrylamide gels*, and molecules from 500 nucleotides to 20 kb on *agarose gels*.

Two methods are common for visualizing separated DNA bands on a gel. If the DNA is not radiolabeled, the gel is incubated in a solution containing the fluorescent dye ethidium:



This planar molecule binds to DNA by intercalating between the base pairs. Binding concentrates ethidium in the DNA and also increases its intrinsic fluorescence. As a result, when the gel is illuminated with ultraviolet light, the regions of the gel containing DNA fluoresce much more brightly than the regions of the gel without DNA ([Figure 7-23a](#)).

Radioactively labeled DNA can be visualized by autoradiography of the gel. In this case, the gel is laid against a sheet of photographic film in the dark, exposing the film at the positions where labeled DNA is present. When the film is developed, a photographic image of the DNA is observed ([Figure 7-23b](#)). Radiolabeled DNA bands also can be detected by laying the gel against a phosphorimager screen, which counts β particles released by labeled molecules in the gel. The resulting data is stored by a computer and can be converted into an image of the gel that looks much like an autoradiogram. [↑ TOP](#)

Multiple Restriction Sites Can Be Mapped on a Cloned DNA Fragment

In addition to separating restriction fragments of different lengths, gel electrophoresis provides a means for estimating the length of fragments. As we've seen, the distance that a restriction fragment migrates in a gel is inversely proportional to the logarithm of its length. Thus the length of a restriction fragment can be determined fairly accurately by comparison with restriction fragments of known length subjected to electrophoresis on the same gel (see [Figure 7-23a](#)).

The ability to determine the length of restriction fragments makes it possible to locate the positions of restriction sites relative to one another on a DNA molecule (e.g., a newly cloned DNA fragment). A diagram showing the positions of restriction sites on a DNA molecule is called a *restriction map*, and the process of determining these positions is called *restriction-site mapping*. [Figure 7-24](#) illustrates the procedure for mapping two restriction sites relative to each other when only *one* copy of each site is

present in a fragment. In this simple case, three fragment samples are digested: one with enzyme I, one with enzyme II, and one with both enzymes.

When a DNA fragment contains *multiple* copies of the recognition site for one or more restriction enzymes, the mapping procedure is more complicated. In this case, the sites for each enzyme must be mapped before the sites for different enzymes can be mapped relative to one another. The first step in this procedure is radiolabeling the 5' ends of both strands of the fragment with [γ - 32 P]ATP and polynucleotide kinase (see [Figure 7-20](#)). As shown in [Figure 7-25](#), the doubly end-labeled fragment is treated with a restriction enzyme that cuts the fragment just once, and the resulting singly end-labeled fragments are separated. These fragments then are partially digested with the enzyme whose multiple recognition sites are being mapped.

Multiple restriction sites in a cloned DNA fragment can be mapped by use of these two methods with multiple restriction enzymes. Because each distinct DNA sequence has a characteristic restriction-site map, such maps can be used to align partially overlapping cloned DNA fragments (see [Figure 7-13](#)). Also, specific small regions within a large cloned DNA fragment can be prepared by digesting the cloned fragment with various combinations of restriction enzymes; the smaller subfragments then can be isolated by gel electrophoresis. [↑ top](#)

Pulsed-Field Gel Electrophoresis Separates Large DNA Molecules

The gel electrophoretic techniques described so far can resolve DNA fragments up to ≈ 20 kb in length. Larger DNAs, ranging from 2×10^4 to 10^7 base pairs [20 kb to 10 megabases (Mb)] in length, can be separated by size with *pulsed-field gel electrophoresis*. This technique depends on the unique behavior of large DNAs in an electric field that is turned on and off (pulsed) at short intervals.

When an electric field is applied to large DNA molecules in a gel, the molecules migrate in the direction of the field and also stretch out lengthwise. If the current then is stopped, the molecules begin to "relax" into random coils. The time required for relaxation is directly proportional to the length of a molecule. The electric field then is reapplied at 90° or 180° to the first direction. Longer molecules relax less than shorter ones during the time the current is turned off. Since the molecules must relax into a random coil before moving off in a new direction, longer molecules start moving in the direction imposed by the new field more slowly than shorter ones. Repeated alternation of the field direction gradually forces large DNA molecules of different size farther and farther apart.

Pulsed-field gel electrophoresis is very important for purifying long DNA molecules up to $\approx 10^7$ base

pairs in length (Figure 7-26). The technique is required for analyzing cellular chromosomes, which range in size from about 5×10^5 base pairs (smallest yeast chromosomes) to $2 - 3 \times 10^8$ base pairs (animal and plant chromosomes). Very large chromosomes must be digested into fragments of 10^7 base pairs or less before they can be analyzed. Such large restriction fragments can be generated with restriction enzymes that cut at rarely occurring 8-bp restriction sites. [↑ top](#)

Purified DNA Molecules Can Be Sequenced Rapidly by Two Methods

Virtually all the information required for the growth and development of an organism is encoded in the DNA of its genome. The availability of techniques to produce and separate DNA restriction fragments a few hundred nucleotides long led to development of two procedures for determining the exact nucleotide sequence of stretches of DNA up to ≈ 500 nucleotides long. These DNA sequencing methods, together with the technology for constructing a library representing the entire genome of an organism, make it possible to determine the exact sequence of the entire DNA of that organism.

The total genomes of many viruses, several bacteria and archaeans, the yeast *S. cerevisiae*, and the roundworm *C. elegans* have already been sequenced. Automation of the techniques for sequencing DNA and computerized storage of the sequence data are facilitating the current effort to determine the sequence of the entire human genome. Within the next decade, if not sooner, researchers also are likely to complete sequencing the entire genomes of the fruit fly *Drosophila melanogaster*, the mouse, and other important experimental organisms. Knowledge of these DNA sequences will undoubtedly revolutionize our understanding of how cells and organisms function.

Maxam-Gilbert Method

In the late 1970s, A. M. Maxam and W. Gilbert devised the first method for sequencing DNA fragments containing up to ≈ 500 nucleotides. In this method, four samples of an end-labeled DNA restriction fragment are chemically cleaved at different specific nucleotides. The resulting subfragments are separated by gel electrophoresis, and the labeled fragments are detected by autoradiography. As illustrated in Figure 7-27, the sequence of the original end-labeled restriction fragment can be determined directly from parallel electrophoretograms of the four samples. [↑ top](#)

Sanger (Dideoxy) Method

A few years later, F. Sanger and his colleagues developed a second method of DNA sequencing, which now is used much more frequently than the Maxam-Gilbert method. The Sanger method is also

called *dideoxy sequencing* because it involves use of 2',3'-dideoxynucleoside triphosphates (ddNTPs), which lack a 3'-hydroxyl group (Figure 7-28). In this method, the single-stranded DNA to be sequenced serves as the template strand for in vitro DNA synthesis; a synthetic 5'-end-labeled oligodeoxynucleotide is used as the primer.

As shown in Figure 7-29, four separate polymerization reactions are performed, each with a low concentration of one of the four ddNTPs in addition to higher concentrations of the normal deoxynucleoside triphosphates (dNTPs). In each reaction, the ddNTP is randomly incorporated at the positions of the corresponding dNTP; such addition of a ddNTP terminates polymerization because the absence of a 3' hydroxyl prevents addition of the next nucleotide. The mixture of terminated fragments from each of the four reactions is subjected to gel electrophoresis in parallel; the separated fragments then are detected by autoradiography. The sequence of the original DNA template strand can be read directly from the resulting autoradiogram (see Figure 7-29c). Once the sequence for a particular cloned DNA fragment is determined, primers for overlapping fragments can be chemically synthesized based on that sequence. The sequence of a long continuous stretch of DNA thus can be determined by individually sequencing the overlapping cloned DNA fragments that compose it. ↑ TOP

SUMMARY

- Generally, to isolate a DNA clone encoding a protein of interest, it is uniquely identified in a collection of a large number of different clones, such as a total genomic library or a cDNA library. Two common identification methods are (1) hybridization to a radiolabeled DNA probe specific for the clone and detection by autoradiography and (2) expression of the encoded protein and detection of the expressed protein by its biochemical activity or by its binding to a radiolabeled antibody specific for the protein.
- A specific hybridization probe for cloned DNA encoding a protein of interest can be prepared based on a short portion of the amino acid sequence of the protein. Use of a degenerate probe, which is a mixture of all the possible DNA sequences that can encode the determined amino acid sequence, ensures that the radiolabeled probe contains the one sequence exactly complementary to the gene of interest (see Figure 7-19). When this perfectly complementary radiolabeled DNA probe hybridizes to DNA from the specific clone of interest on a replica filter, it can be detected by autoradiography (see Figure 7-18).
- Vast numbers of partial cDNA sequences, or expressed sequence tags (ESTs), from humans and various model organisms are stored in computer databases. If a partial amino acid sequence is determined from an isolated protein, the EST database can be searched for an EST (i.e., a partial cDNA sequence) that encodes it. If found, the EST sequence can be used to prepare a perfectly complementary probe for isolation of the corresponding full-length cDNA from a

cDNA library.

- λ expression vectors are designed to express the protein encoded in cloned DNA fragments in *E. coli* cells infected with the vector. Plaques producing the encoded polypeptide can be detected with labeled molecules (e.g., an antibody) that bind to the protein of interest with high affinity (see [Figure 7-21](#)).
- Gel electrophoresis separates DNA (and RNA) molecules according to their size. Consequently, a cloned DNA fragment, released from its cloning vector by digestion with the appropriate restriction enzyme, can be separated from the vector DNA by gel electrophoresis.
- The mobility of either a double- or single-stranded DNA molecule during gel electrophoresis is inversely proportional to the logarithm of its length in nucleotides. Thus the size of a DNA molecule of unknown length can be determined by comparison to the electrophoretic migration of molecules of known length.
- DNA molecules from 1 to 2000 nucleotides long are usually separated by electrophoresis in polyacrylamide gels; molecules from 500 nucleotides to 20 kb, by electrophoresis in agarose gels; and molecules from 20 to 10,000 kb, in pulsed-field agarose gels.
- Multiple restriction sites for a particular restriction enzyme can be mapped in cloned DNAs by partially digesting end-labeled DNA molecules and then determining the length of the resulting fragments by gel electrophoresis and autoradiography (see [Figure 7-25](#)).
- Once the cleavage sites for two restriction enzymes have been mapped on a DNA, these sites can be mapped relative to each other by comparing the sizes of DNA fragments generated with each enzyme separately and with both enzymes together (see [Figure 7-24](#)).
- The sequence of a single-stranded DNA molecule can be determined by either the Maxam-Gilbert method or the Sanger dideoxy method. Sequences of up to ≈ 500 nucleotides can be determined on a single gel because DNA molecules up to this length can be separated on polyacrylamide gels when they differ in length by a single nucleotide.

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SECOND EDITION

Recombinant DNA



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The cover illustration, by Maryin Mattelson, symbolizes some of the elements of this book. The DNA double helix is, of course, central to the book, as it is to the cover illustration. The blocks are double-stranded DNA fragments synthesized by the polymerase chain reaction, a technique that has revolutionized the way molecular genetics experiments are done. The number of fragments doubles repeatedly, going off into the distance (see Chapter 6). The coat colors of the mice running down the helix (in the same direction but with opposite polarity!), are changing from albino to chimeric, then chimeric to agouti. These coat color changes show mice in which genetic engineering has been used to knock out a specific gene. The experiment is shown more realistically in Figure 14-9.

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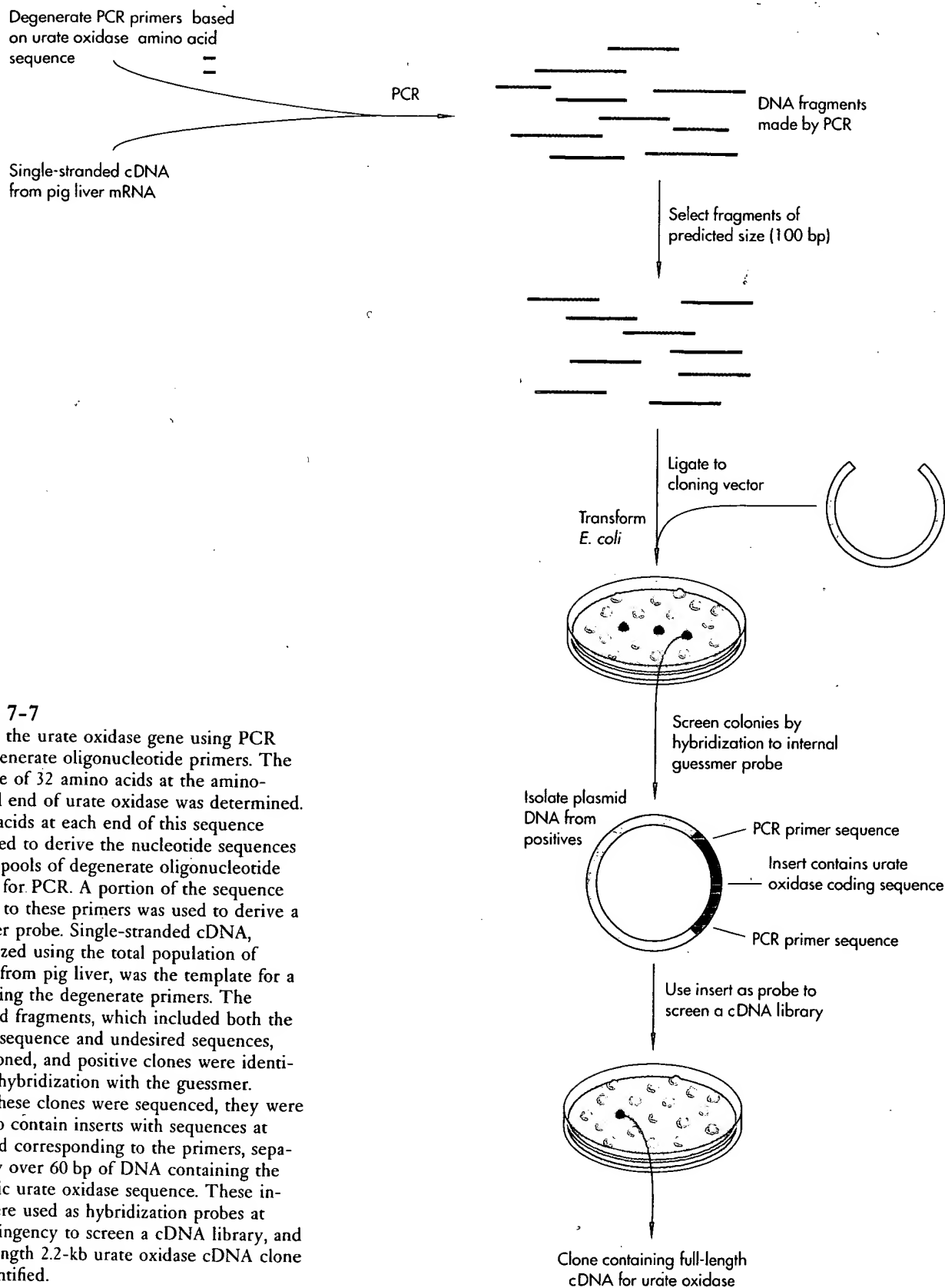


FIGURE 7-7

Cloning the urate oxidase gene using PCR and degenerate oligonucleotide primers. The sequence of 32 amino acids at the amino-terminal end of urate oxidase was determined. Amino acids at each end of this sequence were used to derive the nucleotide sequences for two pools of degenerate oligonucleotide primers for PCR. A portion of the sequence internal to these primers was used to derive a guessmer probe. Single-stranded cDNA, synthesized using the total population of mRNA from pig liver, was the template for a PCR using the degenerate primers. The amplified fragments, which included both the desired sequence and undesired sequences, were cloned, and positive clones were identified by hybridization with the guessmer. When these clones were sequenced, they were found to contain inserts with sequences at each end corresponding to the primers, separated by over 60 bp of DNA containing the authentic urate oxidase sequence. These inserts were used as hybridization probes at high stringency to screen a cDNA library, and a full-length 2.2-kb urate oxidase cDNA clone was identified.